

&lt;!--StartFragment--&gt;RESULT 6

AGLA\_RHIME

ID AGLA\_RHIME Reviewed; 551 AA.  
AC Q9Z3R8;  
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.  
DT 02-NOV-2001, sequence version 2.  
DT 24-JUL-2007, entry version 44.  
DE Probable alpha-glucosidase (EC 3.2.1.20).  
GN Name=aglA; OrderedLocusNames=R00698; ORFNames=SMc03064;  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=99328961; PubMed=10400573;  
RA Willis L.B., Walker G.C.;  
RT "A novel Sinorhizobium meliloti operon encodes an alpha-glucosidase  
RT and a periplasmic-binding-protein-dependent transport system for  
RT alpha-glucosides.";  
RL J. Bacteriol. 181:4176-4184(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,  
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont  
RT Sinorhizobium meliloti strain 1021.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-  
CC linked alpha-D-glucose residues with release of alpha-D-glucose.  
CC -!- SIMILARITY: Belongs to the glycosyl hydrolase 13 family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
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CC -----  
DR EMBL; AF045609; AAD12047.1; -; Genomic\_DNA.  
DR EMBL; AL591784; CAC45270.1; -; Genomic\_DNA.  
DR HSSP; P21332; 1UOK.  
DR GenomeReviews; AL591688\_GR; R00698.  
DR KEGG; sme:SMc03064; -.  
DR BioCyc; SMEL266834:SMC03064-MONOMER; -.  
DR GO; GO:0004558; F:alpha-glucosidase activity; IEA:EC.  
DR InterPro; IPR006047; Glyco\_hydro\_13\_cat.  
DR InterPro; IPR006589; Glyco\_hydro\_13\_sub\_cat.  
DR InterPro; IPR013781; Glyco\_hydro\_cat.  
DR Gene3D; G3DSA:3.20.20.80; Glyco\_hydro\_cat; 1.  
DR Pfam; PF00128; Alpha-amylase; 1.  
DR SMART; SM00642; Amy; 1.  
PE 3: Inferred from homology;  
KW Complete proteome; Glycosidase; Hydrolase.  
FT CHAIN 1 551 Probable alpha-glucosidase.  
FT /FTId=PRO\_0000054312.  
FT ACT\_SITE 212 212 Nucleophile (By similarity).  
FT ACT\_SITE 272 272 Proton donor (By similarity).  
FT ACT\_SITE 345 345 By similarity.  
FT CONFLICT 13 13 P -> A (in Ref. 1).

Query Match 54.5%; Score 1595.5; DB 1; Length 551;  
Best Local Similarity 57.3%; Pred. No. 9.7e-113;  
Matches 294; Conservative 74; Mismatches 130; Indels 15; Gaps 6;

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